STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/553,305_

Source: _PCT/10_

Date Processed by STIC: _10/25/05_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
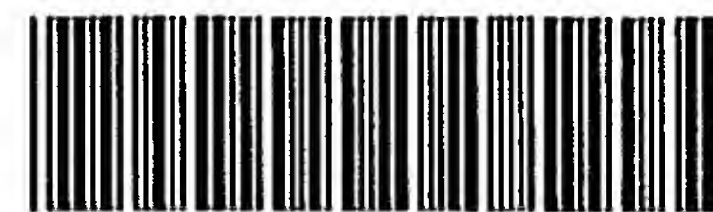Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: 10/553,305 |

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use **space characters**, instead.

4 _____ Non-ASCII — The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5 _____ Variable Length — Sequence(s) _____ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 _____ Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)　　　SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

10 _____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220> — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n/Xaa — "n" can **only** represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

AMC – Biotechnology Systems Branch – 09/09/2003

```
        RAW SEQUENCE LISTING                    DATE: 10/25/2005
        PATENT APPLICATION:   US/10/553,305     TIME: 10:08:24

             Input Set : A:\sequence_listing.txt
             Output Set: N:\CRF4\10252005\J553305.raw
```

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

```
     155 <210> SEQ ID NO: 5   IS shown below
     156 <211> LENGTH: (5)
     157 <212> TYPE: PRT
     158 <213> ORGANISM: Artificial
     160 <220> FEATURE:
     161 <223> OTHER INFORMATION: (Linker)   what is the source of genetic material?
     163 <400> SEQUENCE: 5                    ( see item 11 on
     164 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser    Error
E--> 165 1               5                   10              15        Summary
     273 <210> SEQ ID NO: 15                                             Sheet)
     274 <211> LENGTH: (20) 36 (p.2)
     275 <212> TYPE: DNA                     Please
     276 <213> ORGANISM: Artificial          correct this
     278 <220> FEATURE:
     279 <223> OTHER INFORMATION: Primer      in subsequent
     281 <220> FEATURE:                       sequences
     282 <221> NAME/KEY: misc_feature
     283 <222> LOCATION: 24
     284 <223> OTHER INFORMATION: i
     286 <220> FEATURE:
     287 <221> NAME/KEY: misc_feature
     288 <222> LOCATION: 25
     289 <223> OTHER INFORMATION: i
     291 <220> FEATURE:
     292 <221> NAME/KEY: misc_feature
     293 <222> LOCATION: 29
     294 <223> OTHER INFORMATION: i
     296 <220> FEATURE:
     297 <221> NAME/KEY: misc_feature
     298 <222> LOCATION: 30
```

P.2

RAW SEQUENCE LISTING   DATE: 10/25/2005
PATENT APPLICATION: US/10/553,305   TIME: 10:08:24

Input Set : **A:\sequence_listing.txt**
Output Set: **N:\CRF4\10252005\J553305.raw**

```
      299 <223> OTHER INFORMATION: i    /
      301 <220> FEATURE:
      302 <221> NAME/KEY: misc_feature
      303 <222> LOCATION: 34
      304 <223> OTHER INFORMATION: i    /
      306 <220> FEATURE:
      307 <221> NAME/KEY: misc_feature
      308 <222> LOCATION: 35           /
      309 <223> OTHER INFORMATION: i
      311 <400> SEQUENCE: 15
E-->  312 ggccacgcgt cgactagtac gggnngggnn gggnng                    (36)
      612 <210> SEQ ID NO: 34  ← last sequence in submitted file
      613 <211> LENGTH: (66)
      614 <212> TYPE: PRT                   ) S shown below
      615 <213> ORGANISM: Artificial
      617 <220> FEATURE:
      618 <223> OTHER INFORMATION: (Primer)
      620 <400> SEQUENCE: 34
      621 Gly Gly Gly Gly Ser
E-->  622 1               5
```

a primer is <u>not</u> a peptide
(please give <u>source</u> of genetic material
as explanation)

<210> 10
<211> 18
<212> DNA
<213> Artificial

<400> 10
gcttgccggg tgggccac

Needs explanation *(see p.4)* *for error explanation*

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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 10/25/2005
PATENT APPLICATION: US/10/553,305   TIME: 10:08:25

Input Set : **A:\sequence_listing.txt**
Output Set: **N:\CRF4\10252005\J553305.raw**

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,28,29,30,31,32,33,34

Use of <220> Feature(NEW RULES): *error Explanation*
Sequence(s)__ are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
or"Unknown". Please explain source of genetic material in <220> to <223>
section (See "Federal Register," 6/01/98, Vol. 63, No. 104,pp.29631-32)
(Sec.1.823 of new Rules)

Seq#:10

Input Set : **A:\sequence_listing.txt**
Output Set: **N:\CRF4\10252005\J553305.raw**

```
L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:10 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:26 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:24
L:99 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:97
L:165 M:252 E: No. of Seq. differs, <211> LENGTH:Input:5 Found:15 SEQ:5
L:226 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:10, <213>
ORGANISM:Artificial
L:226 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:10, <213>
ORGANISM:Artificial
L:226 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:226
L:312 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:312 M:252 E: No. of Seq. differs, <211> LENGTH:Input:20 Found:36 SEQ:15
L:622 M:252 E: No. of Seq. differs, <211> LENGTH:Input:66 Found:5 SEQ:34
L:12 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (27) Counted (34)
```